SEQUENCE LISTING

<110> Allen, Keith D.

<120> TRANSGENIC MICE CONTAINING INWARDLY
RECTIFYING POTASSIUM CHANNEL (Kir5.1) GENE DISRUPTIONS

<130> R-902

<150> US 60/254,888
<151> 2000-12-11

<160> 4

<170> FastSEQ for Windows Version 4.0

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<212> DNA
<213> Mus musculus

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Tyr Pro Gly Tyr Pro Pro Glu His Ala Ile Ala Glu Lys Arg Arg Ala
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Arg Arg Arg Leu Leu His Lys Asp Gly Ser Cys Asn Val Tyr Phe Lys
35 40 45
His Ile Phe Gly Glu Trp Gly Ser Tyr Met Val Asp Ile Phe Thr Thr
50 55 60
Leu Val Asp Thr Lys Trp Arg His Met Phe Ile Ile Phe Ser Leu Ser

65 70 75 80
Tyr Ile Leu Ser Trp Leu Ile Phe Gly Ser Ile Phe Trp Leu Ile Ala
85 90 95
Phe His His Gly Asp Leu Leu Ser Asp Pro Asp Ile Thr Pro Cys Val
100 105 110
Asp Asn Val His Ser Phe Thr Ala Ala Phe Leu Phe Ser Leu Glu Thr
115 120 125
Gln Thr Thr Ile Gly Tyr Gly Tyr Arg Cys Val Thr Glu Glu Cys Ser
130 135 140
Val Ala Val Leu Thr Val Ile Leu Gln Ser Ile Leu Ser Cys Ile Ile
145 150 155 160
Asn Thr Phe Ile Ile Gly Ala Ala Leu Ala Lys Met Ala Thr Ala Arg
165 170 175
Lys Arg Ala Gln Thr Ile Arg Phe Ser Tyr Phe Ala Leu Ile Gly Met
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Arg Asp Gly Lys Pro Cys Leu Met Trp Arg Ile Gly Asp Phe Arg Pro
195 200 205
Asn His Val Val Glu Gly Thr Val Arg Ala Gln Leu Leu Arg Tyr Ser
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Glu Asp Ser Glu Gly Arg Met Thr Met Ala Phe Lys Asp Leu Lys Leu
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Val Asn Asp Gln Ile Ile Leu Val Thr Pro Val Thr Ile Val His Glu
245 250 255
Ile Asp His Glu Ser Pro Leu Tyr Ala Leu Asp Arg Lys Ala Val Ala
260 265 270
Lys Asp Asn Phe Glu Ile Leu Val Thr Phe Ile Tyr Thr Gly Asp Ser
275 280 285
Thr Gly Thr Ser His Gln Ser Arg Ser Ser Tyr Ile Pro Arg Glu Ile
290 295 300
Leu Trp Gly His Arg Phe His Asp Val Leu Glu Val Lys Arg Lys Tyr
305 310 315 320
Tyr Lys Val Asn Cys Leu Gln Phe Glu Gly Ser Val Glu Val Tyr Ala
325 330 335
Pro Phe Cys Ser Ala Lys Gln Leu Asp Trp Lys Asp Gln Gln Leu Asn
340 345 350
Asn Leu Glu Lys Thr Ser Pro Ala Arg Gly Ser Cys Asn Ser Asp Thr
355 360 365
Asn Thr Arg Arg Arg Ser Phe Ser Ala Val Ala Val Val Ser Ser Cys
370 375 380
Glu Asn Pro Glu Glu Thr Val Leu Ser Pro Gln Asp Glu Cys Lys Glu
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gaccatacgc ttcagctatt ttgccctcat tggtatgaga gacgggaagc tttgcctcat 180
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